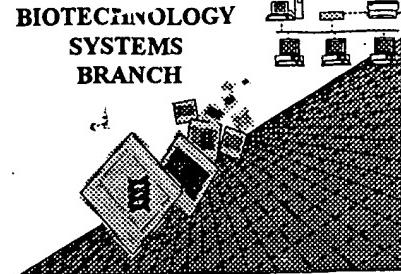


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762,267
Source: Pct/09
Date Processed by STIC: 7/11/2001

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,767

DATE: 07/11/2001
TIME: 11:19:54

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07112001\I762767.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:
C--> 3 (i) APPLICANT:

SCHMIDT, Harald
ZABEL, Ulrike
POLLER, Wolfgang

W--> 8 (ii) TITLE OF INVENTION: Isolated and purified human soluble
guanylyl cyclase al/al (hsGCa1/al)

E--> 10 (iii) VOS-101
11 (iv) US 09/762,767

W--> 12 2001-02-13

W--> 13 (iv) PCT/DE99/02601

W--> 14 1999-08-16

W--> 15 (iv) DE 198 37 015.6

W--> 16 1998-08-14

E--> 22 (iii) NUMBER OF SEQUENCES: 10

C--> 24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

C--> 0 (vi) CURRENT APPLICATION DATA:

C--> 0 (A) APPLICATION NUMBER: US/09/762,767

C--> 0 (B) FILING DATE: 13-Feb-2001

ERRORED SEQUENCES

E--> 30 (2) DATA TO SEQ ID NO: 1:

E--> 0 (2) INFORMATION FOR SEQ ID NO:

31 (i) SEQUENCE CHARACTERISTICS:

32 (A) LENGTH: 3015 basepairs

33 (B) TYPE: nucleotide

34 (C) STRANDEDNESS: doublestrand

35 (D) TOPOLOGY: linear

37 (ii) MOLECULE TYPE: genomic DNA

0 (D) DEVELOPMENTAL STAGE: 1:

E--> 39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

41	CCCTTATGGC GATTGGCGG CTGCAGAGAC CAGGACTCAG TTCCCCTGCC CTAGTCTGAG	60
42	CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTCCAGAA GCAGGTTCA GTGCAGAGTT	120
43	TTCCTACACT TTTCCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGCAGGAGGAC	180
44	ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGCG TGATCTCACC	240
45	ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG	300
46	GTGTGCGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG	360
47	TCTCCGCGCC TGTCTGCACC CTGTCGCCTG AGCTGCCTGA CAGTGACAAT GACATCCCAG	420
48	TTACCAAGTGT CCTTGAATTG ATAGTGGCTT CTGTTGTCA GTCTCATATA AGAACTACAG	480
49	CTCATCAGGA GGAGATCGCA GCAGGGTAAG AGACACCAAC ACCATGTTCT GCACGAAGCT	540

Completely invalid
format for
a U.S.
case.
(See attached)

EPO format is
invalid for U.S.
case

09/762,767 1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

SCHMIDT, Harald
ZABEL, Ulrike
POLLER, Wolfgang

[Delete]

(ii) TITLE OF THE INVENTION: Isolated and purified human soluble guanylyl cyclase al/^β1 (hsGCa1/^β1)

(iii) YES-101 →

NUMBER OF SEQUENCES: (← insert third and delete all accent marks - they cannot be processed in the CRF)

(vi) US 09/762,767
2001-02-13

goes under CURRENT APPLICATION DATA

response be processed in the CRF

(vii) PCT/DE99/02601
1999-08-16

Move

(viii) DE 198 37 015.6
1998-08-14

These (go under Prior Application Data)

(iii) → NUMBER OF SEQUENCES: 10

(j) → COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 ((EPA))

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

INFORMATION FOR SEQ ID NO: 1: →

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3015 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: doublestrand
- (D) TOPOLOGY: linear

((C)) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

((D)) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTTATGGC GATTGGCGG CTGCAGAGAC CAGGACTCAG TTCCCCTGCC CTAGTCTGAG	60
CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTCCAGAA GCAGGTTCA GTGCAGAGTT	120
TTCCTACACT TTTCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGCGGAGGAC	180
ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGGCG TGATCTCACC	240
ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG	300
GTGTGCGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCG	360
TCTCCGCGCC TGTCTGCACC CTGTCGCTG AGCTGCTGA CAGTGACAAT GACATCCCAG	420
TTACCACTGT CCTTGAATTG ATAGTGGCTT CTGTTTGTC GTCTCATATA AGAACTACAG	480
CTCATCAGGA GGAGATCGCA GCAGGGTAAG AGACACCAAC ACCATGTTCT GCACGAAGCT	540
CAAGGATCTC AAGATCACAG GAGAGTGTCC TTTCTCTTA CTGGCACCAAG GTCAAGTTCC	600
TAACGAGTCT TCAGAGGAGG CAGCAGGAAG CTCAGAGAGC TGCAAAGCAA CCGTCCCCAT	660
CTGTCAGAAC ATTCCCTGAGA AGAACATACA AGAAAGTCTT CCTCAAAGAA AAACCAGTCG	720
GAGCCGAGTC TATCTTCACA CTTTGGCAGA GAGTATTGCA AACTGATT TCCCAGAGTT	780
TGAACGGCTG AATGTTGCAC TTCAGAGAAC ATTGGCAAAG CACAAAATAA AAGAAAGCAG	840
GAAATCTTG GAAAGAGAAC ACTTTGAAAA AACAAATTGCA GAGCAAGCAG TTGCAGCAGG	900
AGTTCCAGTG GAGGTTATCA AAGAATCTCT TGGTGAAGAG GTTTTAAAAA TATGTTACGA	960
GGAAGATGAA AACATCCTTG GGGTGGTTGG AGGCACCCCTT AAAGATTTT TAAACAGCTT	1020

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CAGTACCCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAAGCA	GGAAAAAGGG	GCAGGCTTGA	1080
GGACGCCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATTTT	CTACATGTTT	ACTACTTCTT	1140
CCCTAACAGA	ACCACCTCCC	TGATTCTTCC	CGGCATCATA	AAGGCAGCTG	CTCACGTATT	1200
ATATGAAACG	GAAGTGGAAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	ATTGCAGCGA	1260
GTTTGTGAAT	CAGCCCTACT	TGTTGTACTC	CGTTCACATG	AAAAGCACCA	AGCCATCCCT	1320
GTCCCCCAGC	AAACCCAGT	CCTCGCTGGT	GATTCCCACA	TCGCTATTCT	GCAAGACATT	1380

delete all hard page
 breaks

09/262,767 3

TCCATTCCAT	TTCATGTTG	ACAAAGATAT	GACAATTCTG	CAATTGGCA	ATGGCATCAG	1440
AAGGCTGATG	AACAGGAGAG	ACTTCAAGG	AAAGCCTAAT	TTTGAAGAAT	ACTTTGAAAT	1500
TCTGACTCCA	AAAATCAACC	AGACGTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	1560
TGTTGTACGA	GTGAGGAGAT	GGGACAAC	TGTGAAGAAA	TCTTCAGGG	TTATGGACTT	1620
CAAAGGCCAA	ATGATCTACA	TTGTTGAATC	CAGTGCAATC	TTGTTTTGG	GGTCACCC	1680
TGTGGACAGA	TTAGAAGATT	TTACAGGACG	AGGGCTCTAC	CTCTCAGACA	TCCCATTCA	1740
CAATGCACTG	AGGGATGTGG	TCTTAATAGG	GGAACAAGCC	CGAGCTCAAG	ATGGCCTGAA	1800
GAAGAGGCTG	GGGAAGCTGA	AGGCTACCC	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	1860
GAAGAAAAAG	ACAGTAGACCC	TTCTGTGCTC	CATATTCCC	TGTGAGGTTG	CTCAGCAGCT	1920
GTGGCAAGGG	CAAGTTGTGC	AAGCCAAGAA	GTTCAGTAAT	GTCACCATGC	TCTTCTCAGA	1980
CATCGTTGGG	TTCACTGCCA	TCTGCTCCC	GTGCTCACCG	CTGCAGGTCA	TCACCATGCT	2040
CAATGCACTG	TACACTCGCT	TCGACCAGCA	GTGTGGAGAG	CTGGATGTCT	ACAAGGTGGA	2100
GACCATTGGC	GATGCCTATT	GTGTAGCTGG	GGGATTACAC	AAAGAGAGTG	ATACTCATGC	2160
TGTTCAGATA	GCGCTGATGG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	2220
CCATGGAGAA	CCTATCAAGA	TGCGAATTGG	ACTGCACTCT	GGATCAGTTT	TTGCTGGCGT	2280
CGTTGGAGTT	AAAATGCC	GTTACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2340
ATTTGAGTCC	TGCA	GTTACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2400
CAAAGACTGT	CCTGGTTTCG	TGTTTACCC	TCGATCAAGG	GAGGAAC	TTGCTGGCGT	2460
CCCTAGTGAA	ATCCCCGGAA	TCTGCCATT	TCTGGATGCT	TACCAACAAG	AAACAAACTC	2520
AAAACCATGC	TTCCAAAAGA	AAGATGTGGA	AGATGGCAAT	GCCAA	TAGGCAAAGC	2580
ATCAGGAATA	GATTAGCAAC	CTATATAACCT	ATTTATAAGT	CTTGGGGTT	TGACTCAT	2640
AAGATGTGTA	GAGCCTCTGA	AAGCACTTTA	GGGATTGTAG	ATGGCTAAC	AGCAGTATT	2700
AAATTCAGG	AGCCAAGTCA	CAATCTTCT	CCTGTTAAC	ATGACAA	ATGACAA	2760
CAGTACTTCA	GCTCTTCAAG	AAAAAA	AAACCTTAA	AAGCTACT	TGTGGGAGTA	2820
TTTCTATTAT	ATAACCAGCA	CTTACTACCT	GTACTCAAA	TTCAGCAC	TGTACATATA	2880
TCAGATAATT	GTAGTCAATT	GTACAAACTG	ATGGAGTCAC	CTGCAATCTC	ATATCCTGGT	2940
GGAATGCCAT	GGTTATTAAA	GTGTGTTGT	GATAGTGTG	TCAAAAAAAA	AAAAAAA	3000
AAAAAAAAAA	AAAAAA					3015

(2) ~~DATA TO SEQ ID NO: 2~~ INFORMATION FOR SEQ ID No: 2!

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al
(hsGCaI)) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

(xi) SEQUENCEDDESCRIPTION: SEQ ID NO: 2:

Met	Phe	Cys	Thr	Lys	Leu	Lys	Asp	Leu	Lys	Ile	Thr	Gly	Glu	Cys	Pro
					5					10					15
Phe	Ser	Leu	Leu	Ala	Pro	Gly	Gln	Val	Pro	Asn	Glu	Ser	Ser	Glu	Glu
					20				25					30	
Ala	Ala	Gly	Ser	Ser	Glu	Ser	Cys	Lys	Ala	Thr	Val	Pro	Ile	Cys	Gln
							35		40				45		
Asp	Ile	Pro	Glu	Lys	Asn	Ile	Gln	Glu	Ser	Leu	Pro	Gln	Arg	Lys	Thr
						50		55				60			
Ser	Arg	Ser	Arg	Val	Tyr	Leu	His	Thr	Leu	Ala	Glu	Ser	Ile	Cys	Lys
						65		70			75				80
Leu	Ile	Phe	Pro	Glu	Phe	Glu	Arg	Leu	Asn	Val	Ala	Leu	Gln	Arg	Thr
						85				90				95	
Leu	Ala	Lys	His	Lys	Ile	Lys	Glu	Ser	Arg	Lys	Ser	Leu	Glu	Arg	Glu
						100			105				110		
Asp	Phe	Glu	Lys	Thr	Ile	Ala	Glu	Gln	Ala	Val	Ala	Ala	Gly	Val	Pro
						115			120				125		
Val	Glu	Val	Ile	Lys	Glu	Ser	Leu	Gly	Glu	Glu	Val	Phe	Lys	Ile	Cys
						130		135				140			
Tyr	Glu	Glu	Asp	Glu	Asn	Ile	Leu	Gly	Val	Val	Gly	Gly	Thr	Leu	Lys
						145		150			155				160
Asp	Phe	Leu	Asn	Ser	Phe	Ser	Thr	Leu	Leu	Lys	Gln	Ser	Ser	His	Cys

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165 170 175
Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys
180 185 190
Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys
195 200 205
Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His
210 215 220
Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe
2225 230 235 240
His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser
245 250 255
Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln
260 265 270
Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe
275 280 285
His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly
290 300 305
Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe
310 315 320 325
Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser
330 335 340
Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg
345 350 355
Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly
360 365 370
Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser
375 380 385
Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu
390 395 400 405
Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly
410 415 420
Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu
425 430 435
Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Lys Lys
440 445 450
Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln
455 460 465
Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val
470 475 480 485
Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln
490 495 500
Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg
505 510 515
Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile
520 525 530
Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr
535 540 545
His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser
550 555 560 565
Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly
570 575 580
Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro
585 590 595
Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu
600 605 610
Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg
615 620 625

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Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu
 630 635 640 645
 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
 650 655 660
 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
 665 670 675
 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly
 680 685 690
 Ile Asp
 695

(2) DATA TO SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2443 basepairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: doublestrand
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCCCCCG	CCGCTGCCGC	CTCTGCCCTGG	GTCCCCTCGG	CCGTACCTCT	CGGTGGGGC	60
TGCCCTCCCCG	GCTCCCGGTG	CAGACACCAT	GTACGGATTT	GTGAATCACCG	CCCTGGAGTT	120
GCTGGTGATC	CGCAATTACG	GCCCCGAGGT	GTGGGAAGAC	ATCAAAAAAG	AGGCACAGTT	180
AGATGAAGAA	GGACAGTTTC	TTGTCAGAAT	AATATATGAT	GACTCCAAAA	CTTATGATTT	240
GGTTGCTGCT	GCAAGCAAAG	TCCTCAATCT	CAATGCTGGA	GAAATCCTCC	AAATGTTGG	300
GAAGATGTT	TTCGTCTTT	GCCAAGAACATC	TGGTTATGAT	ACAATCTTGC	GTGTCTGGG	360
CTCTAATGTC	AGAGAATTC	TACAGAACCT	TGATGCTCTG	CACGACCACC	TTGCTACCAT	420
CTACCCAGGA	ATGCGTGCAC	CTTCCTTTAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
CATTTGCAC	TACTACTCAG	AGAGAGAAGG	ACTTCAGGAT	ATTGTCAATTG	GAATCATCAA	540
AACAGTGGCA	CAACAAATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTTC	AGCAAAGAAA	600
TGAAGAATGT	GATCATACTC	AATTTTAAT	TGAAGAAAAA	GAGTCAAAAG	AAGAGGATT	660
TTATGAAGAT	CTTGACAGAT	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
TACATTCTGC	AAAGCTTTTC	CTTTTCATAT	AATATTGAC	CGGGACCTAG	TGGTCACTCA	780
GTGTGGCAAT	GCTATATACA	GAGTTCTCCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
GTCTGTCTTC	TCGCTGGTTC	GTCCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTCTCA	900
CATCAAACT	GTTTTGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
ATGTGAGGAT	GAACTGACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
CTACTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTCA	TGAACCTGG	1080
CGATTGACA	AGGAGAGGGC	TGTATCTAACG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
TCTTGTCTT	TTGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCCAAG	AACTGGAAAT	1200
CCTCACTGAC	AGGCTACAGC	TCACGTTAAG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
CACATTGCTG	TATTCTGTCC	TTCCCTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
AGTGCCTGCC	AAAAGATATG	ACAATGTGAC	CATCCTCTT	AGTGGCATTG	TGGGCTTCAA	1380
TGCTTCTGT	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
CGACCTCTAC	ACCAAGATTG	ACACACTGAC	TGATTCCCGG	AAAAACCCAT	TTGTTTATAA	1500
GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAAGAGC	CATGCATTCA	1560
CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
AGTAGATGGT	GAATCTGTC	AGATAACAAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
TGTCATAGGA	CAGCGGATGC	CTCGATACTG	TCTTTTGGG	AATACTGTCA	ACCTCACAAG	1740
CCGAACAGAA	ACCACAGGAG	AAAAGGGAAA	AATAAAATGTG	TCTGAATATA	CATACAGATG	1800
TCTTATGTCT	CCAGAAAATT	CAGATCCACA	ATTCCACTG	GAGCACAGAG	GCCCAGTGTG	1860
CATGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTCTA	TCCAGAAAAA	ATACAGGAAC	1920
AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGGATTAT	GGGGTGAAGA	GGAGTACAGA	1980
CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCTTC	CCTATGGATA	2040
CAGATTTCT	TTTGTCTTG	TCCATTACCC	CAAGACTTTC	TTCTAGATAT	ATCTCTCACT	2100
ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTT	AGGCTTTAGT	ATATTATCTA	2160
AAGTTGGCT	TTTGATGTGG	ATGATGTGAG	CTTCATGTGT	CTTAAAATCT	ACTACAAGCA	2220
TTACCTAAC	TGGTGATCTG	CAAGTAGTAG	GCACCCAATA	AATATTGTT	GAATTTAGTT	2280
AAATGAAACT	GAACAGTGTG	TGGCCATGTG	TATATTATA	TCATGTTAC	CAAATCTGTT	2340

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TAGTGTCCA CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AAGTTTATAT
CATGTTGGTG TATATCCTTA TAGAAATCAT TTTCTAAAGG AGT

2400
2443

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1
(hsGCb1))

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4:

Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn
5 10 15
Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp
20 25 30
Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr
35 40 45
Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly
50 55 60
Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu
65 70 75 80
Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu
85 90 95
Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr
100 105 110
Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly
115 120 125
Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp
130 135 140
Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr
145 150 155 160
Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His
165 170 175
Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr
180 185 190
Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile
195 200 205
Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp
210 215 220
Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu
225 230 235 240
Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu
245 250 255
Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile
260 265 270
Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu
275 280 285
Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu
290 295 300
Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu
305 310 315 320
Phe Leu Cys Ser Pro Ser Val Met Asn Leu Asp Asp Leu Thr Arg Arg
325 330 335
Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
340 345 350
Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
355 360 365
Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu

09/762767 1

370 375 380
Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
385 390 395 400
Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
 405 410 415
Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
 420 425 430
Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
 435 440 445
Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
 450 455 460
Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
465 470 475 480
Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
 485 490 495
Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
 500 505 510
Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
 515 520 525
Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
 530 535 540
Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
545 550 555 560
Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
 565 570 575
Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
 580 585 590
Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
 595 600 605
Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp
 610 615

(2) DATA TO SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCa1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro

 5 10

(2) DATA TO SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn

 5 10 15

Thr Gly Thr Glu Glu Thr

 20

(2) DATA TO SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 basepairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single ~~strands~~
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

(2) DATA TO SEQ ID NO: 8:

- ↑
insert
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG

18

(2) DATA TO SEQ ID NO: 9:

- ↑
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

(2) DATA TO SEQ ID NO: 10:

- ↑
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 basepairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strands
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20

- 1) Please issue all (A) LENGTH responses
reflect actual number of bases or amino acids
- 2) all U.S. applications filed on or after
July 1, 1998 and which cannot claim a
prior application filed before July 1, 1998, need
to be in new sequence header format.